```
OM of: US-09-805-550-4 to: N_Geneseq_032802:*   out_format : pfs

Date: Aug 31, 2002  7:41 AM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
 -MODEL=frame+_p2n.model -DEV=x1h
 -Q=/cgn2_1/USPTO_spool/US09805550/runat_29082002_160820_307/app_query.fasta_1.897
 -DB=N_Geneseq_032802 -QFMT=fastap -SUFFIX=oligop2n.rng
 -GAPOP=4.500 -GAPEXT=0.050 -MINMATCH=0.100 -LOOPCL=0.000
 -LOOPEXT=0.000 -QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=60.000
 -XGAPEXT=60.000 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=60.000
 -YGAPEXT=60.000 -DELOP=6.000 -DELEXT=7.000 -START=1
 -MATRIX=oligo -TRANS=human40.cdi -LIST=45 -DOCALIGN=200
 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
 -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
 -USER=US09805550_@CGN1_1_0 -NCPU=6 -ICPU=3 -LONGLOG
 -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1

Search information block:
Query: US-09-805-550-4
Query length: 368
Database: N_Geneseq_032802:*
Database sequences: 1736436
Database length: 858457221
Search time (sec): 297.440000

WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP=XGAPOP=60.000
WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.000


score_list:
Sequence            Strd Orig    ZScore    EScore Len  ! Documentation  ..
/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:AAD01231 +  368.00 6631.44  0.0       17
/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:AAC37705 +   21.00  351.55  3.1e-11   15
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AC   AAD01231;
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DT   04-OCT-2000  (first entry)
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DE   Maize Rad23 protein #2 encoding cDNA.
XX
KW   Rad23; maize; ATCC No: PTA-531; recombinant expression cassette; wheat;
KW   transgenic plant; soybean; sunflower; sorghum; canola; modulator; ss.
XX
OS   Zea mays.
XX
FH   Key             Location/Qualifiers
FT   CDS             106..1222
FT                   /*tag=  a
FT                   /product= "Maize Rad23 protein #2"
FT                   /note= "Contained in ATCC No: PTA-531"
XX
PN   WO200031268-A1.
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PD   02-JUN-2000.
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PF   12-OCT-1999;   99WO-US24129.
XX
PR   23-NOV-1998;   98US-0109728.
XX
PA   (PION-) PIONEER HI-BRED INT INC.
XX
PI   Mahajan PB,  Tagliani L;
XX
DR   WPI; 2000-400078/34.
DR   P-PSDB; AAY71459.
XX
PT   Isolated nucleic acid encoding maize RAD23 protein is used to modulate
PT   the levels of polypeptides in plant or in assays for identifying
PT   compounds that bind to and/or increase/decrease enzymatic activity of
PT   catalytically active polypeptides -
XX
PS   Claim 1e; Page 76-78; 82pp; English.
XX
CC   The present sequence is the cDNA encoding maize Rad23 protein #2. It is
CC   isolated from a Zea mays cell line, B73 callus tissue regenerated five
CC   days after transfer of the callus from medium containing auzin to a
CC   medium devoid of exogenous auxin. This cDNA is deposited under the ATCC
CC   No: PTA-531. Maize Rad23 DNA sequence operably linked to a promoter, can
CC   be used to construct a recombinant expression cassette. This expression
CC   cassette can be used to generate a dicot or monocot transgenic plant
CC   e.g., maize, soybean, sunflower, sorghum, canola, wheat, etc,. It can
CC   also be used to modulate the levels of Rad23 polypeptide expression in a
CC   plant or in assays to identify compounds, that bind to and/or modulate
CC   the enzymatic activity of catalytically active polypeptides.
XX
SQ   Sequence 1702 BP; 490 A; 373 C; 432 G; 407 T; 0 other;


alignment_scores:
            Quality:  368.00              Length:    368
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

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    106 ATGAAGCTGACGGTGAAGACCCTCAAGGGAACGCACTTCGAGATCCGGGT 155

     17 lGlnProAsnAspThrIleMetAlaValLysLysAsnIleGluGluIleG 34
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    156 GCAGCCCAACGACACGATTATGGCTGTGAAGAAGAATATAGAAGAGATAC 205

     34 lnGlyLysAspSerTyrProTrpGlyGlnGlnLeuLeuIlePheAsnGly 50
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    206 AAGGGAAAGACAGCTATCCATGGGGCCAACAACTGCTGATTTTCAATGGA 255

     51 LysValLeuLysAspGluSerThrLeuGluGluAsnLysValAsnGluAs 67
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    256 AAGGTCTTGAAAGATGAAAGTACATTGGAAGAGAATAAAGTCAATGAGGA 305

     67 pGlyPheLeuValValMetLeuSerLysGlyLysThrSerGlySerThrG 84
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    306 TGGGTTTCTAGTTGTCATGCTTAGTAAGGGTAAAACATCTGGTTCAACTG 355

     84 lyThrSerSerSerGlnHisSerAsnThrProAlaThrArgGlnAlaPro 100
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    356 GAACTTCATCTTCCCAGCACTCAAACACTCCTGCAACAAGGCAGGCACCT 405

    101 ProLeuGluAlaProGlnGlnAlaProGlnProProValAlaProIleTh 117
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    406 CCTCTAGAGGCCCCACAACAAGCTCCTCAACCCCCGGTGGCACCAATTAC 455

    117 rThrSerGlnProGluGlyLeuProAlaGlnAlaProAsnThrHisAspA 134
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    456 AACTTCTCAGCCTGAAGGACTTCCTGCACAGGCACCTAACACACATGACA 505

    134 snAlaAlaSerAsnLeuLeuSerGlyArgAsnValAspThrIleIleAsn 150
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    151 GlnLeuMetGluMetGlyGlyGlySerTrpAspLysAspLysValGlnAr 167
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    167 gAlaLeuArgAlaAlaTyrAsnAsnProGluArgAlaValGluTyrLeuT 184
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    184 yrSerGlyIleProValThrAlaGluIleAlaValProIleGlyGlyGln 200
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    201 GlyAlaAsnThrThrAspArgAlaProThrGlyGluAlaGlyLeuSerGl 217
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    217 yIleProAsnThrAlaProLeuAspLeuPheProGlnGlyAlaSerAsnA 234
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    234 laGlyGlyGlyAlaGlyGlyGlyProLeuAspPheLeuArgAsnAsnPro 250
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    251 GlnPheGlnAlaValArgGluMetValHisThrAsnProGlnIleLeuGl 267
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    906 GCCTATGCTCGTTGAGTTGAGCAAGCAGAATCCTCAAATTCTAAGGTTGA 955

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   1006 GGCGGAGAGGGGGATTTCTTAGACCAACCTGAGGAGGATGAAATGCCTCA 1055

    317 sAlaIleSerValThrProGluGluGlnGluAlaIleGlyArgLeuGluS 334
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    334 erMetGlyPheAspArgAlaArgValIleGluAlaPheLeuAlaCysAsp 350
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   1106 CCATGGGGTTCGACAGAGCACGCGTTATTGAAGCATTCTTAGCCTGCGAT 1155

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seq_documentation_block:
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DT   17-OCT-2000  (first entry)
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DE   Arabidopsis thaliana DNA fragment SEQ ID NO: 18371.
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KW   Hybridisation assay; genetic mapping; gene expression control;
KW   protein identification; signal transduction pathway;
KW   metabolic pathway; promoter; termination sequence; ss.
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OS   Arabidopsis thaliana.
XX
PN   EP1033405-A2.
XX
PD   06-SEP-2000.
XX
PF   25-FEB-2000; 2000EP-0301439.
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PR   09-MAR-1999;   99US-0123548.
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KW   protein identification; signal transduction pathway;
KW   metabolic pathway; promoter; termination sequence; ss.
XX
OS   Arabidopsis thaliana.
XX
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PD   06-SEP-2000.
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KW   protein identification; signal transduction pathway;
KW   metabolic pathway; promoter; termination sequence; ss.
XX
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XX
PN   EP1033405-A2.
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KW   transgenic plant; soybean; sunflower; sorghum; canola; modulator; ss.
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OS   Zea mays.
XX
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PR   23-NOV-1998;   98US-0109728.
XX
PA   (PION-) PIONEER HI-BRED INT INC.
XX
PI   Mahajan PB,  Tagliani L;
XX
DR   WPI; 2000-400078/34.
DR   P-PSDB; AAY71458.
XX
PT   Isolated nucleic acid encoding maize RAD23 protein is used to modulate
PT   the levels of polypeptides in plant or in assays for identifying
PT   compounds that bind to and/or increase/decrease enzymatic activity of
PT   catalytically active polypeptides -
XX
PS   Claim 1e; Page 73-75; 82pp; English.
XX
CC   The present sequence is the cDNA encoding maize Rad23 protein #1. It is
CC   isolated from V5 root tissue of a Zea mays cell line B73, infested with
CC   corn root worm. This cDNA is deposited under the ATCC No: PTA-530. Maize
CC   Rad23 DNA sequence operably linked to a promoter can be used to construct
CC   a recombinant expression cassette. This expression cassette can be used
CC   to generate a dicot or monocot transgenic plant e.g., maize, soybean,
CC   sunflower, sorghum, canola, wheat, etc,. It can also be used to modulate
CC   the levels of Rad23 polypeptide expression in a plant or in assays to
CC   identify compounds, that bind to and/or modulate the enzymatic activity
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KW   protein identification; signal transduction pathway;
KW   metabolic pathway; promoter; termination sequence; ss.
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XX
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PR   14-MAY-1999;   99US-0134221.
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PR   18-MAY-1999;   99US-0134768.
PR   19-MAY-1999;   99US-0134941.
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PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
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PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.

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PR   26-OCT-1999;   99US-0161361.
PR   28-OCT-1999;   99US-0161920.
PR   28-OCT-1999;   99US-0161992.
PR   28-OCT-1999;   99US-0161993.
PR   29-OCT-1999;   99US-0162142.

alignment_scores:
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              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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 Align seg 1/1  to: AAC43990  from: 1  to: 720

       5 ValLysThrLeuLysGlyThrHisPheGluIle 15
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     130 GTGAAAACTCTCAAGGGGACTCACTTCGAGATC 162

seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:ABL03535

seq_documentation_block:
ID   ABL03535 standard; cDNA; 1477 BP.
XX
AC   ABL03535;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster expressed polynucleotide SEQ ID NO 5087.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical; gene; ss.
XX
OS   Drosophila melanogaster.
XX
PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US09231.
XX
PR   23-MAR-2000; 2000US-191637P.
PR   11-JUL-2000; 2000US-0614150.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Venter JC,  Adams M,  Li PWD,  Myers EW;
XX
DR   WPI; 2001-656860/75.
DR   P-PSDB; ABB59432.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signalling and cell-cell
PT   interactions -
XX
PS   Claim 1; SEQ ID NO 5087; 21pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL01840-ABL16175) and the encoded proteins
CC   (ABB57737-ABB72072).
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 1477 BP; 462 A; 313 C; 298 G; 404 T; 0 other;

alignment_scores:
            Quality:   11.00             Length:     11
              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-805-550-4 x ABL03535   ..

 Align seg 1/1  to: ABL03535  from: 1  to: 1477

     173 TyrAsnAsnProGluArgAlaValGluTyrLeu 183
         |||||||||||||||||||||||||||||||||
     667 TATAACAACCCGGAAAGAGCCGTTGAATATCTC 699

seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:ABL03534

seq_documentation_block:
ID   ABL03534 standard; cDNA; 4198 BP.
XX
AC   ABL03534;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster expressed polynucleotide SEQ ID NO 5084.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical; gene; ss.
XX
OS   Drosophila melanogaster.
XX
PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US09231.
XX
PR   23-MAR-2000; 2000US-191637P.
PR   11-JUL-2000; 2000US-0614150.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Venter JC,  Adams M,  Li PWD,  Myers EW;
XX
DR   WPI; 2001-656860/75.
DR   P-PSDB; ABB59431.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signalling and cell-cell
PT   interactions -
XX
PS   Claim 1; SEQ ID NO 5084; 21pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL01840-ABL16175) and the encoded proteins
CC   (ABB57737-ABB72072).
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 4198 BP; 1397 A; 710 C; 719 G; 1372 T; 0 other;


alignment_scores:
            Quality:   11.00             Length:     11
              Ratio:  1.000               Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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 US-09-805-550-4 x ABL03534/rev   ..

 Align seg 1/1  to reverse of: ABL03534  from: 1  to: 4198

     173 TyrAsnAsnProGluArgAlaValGluTyrLeu 183
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    2391 TATAACAACCCGGAAAGAGCCGTTGAATATCTC 2359

seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:AAT23970

seq_documentation_block:
ID   AAT23970 standard; cDNA to mRNA; 350 BP.
XX
AC   AAT23970;
XX
DT   27-AUG-1996  (first entry)
XX
DE   Human gene signature HUMGS05926.
XX
KW   Gene signature; messenger RNA; mRNA; relative abundance; frequency;
KW   human; cloning; mapping; non-biased library; diagnosis; detection;
KW   cell typing; abnormal cell function; ss.
XX
OS   Homo sapiens.
XX
PN   WO9514772-A1.
XX
PD   01-JUN-1995.
XX
PF   11-NOV-1994;   94WO-JP01916.
XX
PR   12-NOV-1993;   93JP-0355504.
XX
PA   (MATS/) MATSUBARA K.
PA   (OKUB/) OKUBO K.
XX
PI   Matsubara K,  Okubo K;
XX
DR   WPI; 1995-206931/27.
XX
PT   Identifying gene signatures in 3'-directed human cDNA library - e.g.
PT   for diagnosis of abnormal cell function, by preparing cDNA that
PT   reflects relative abundance of corresp. mRNA in specific human
PT   tissues
XX
PS   Claim 1; Page 1499; 2245pp; Japanese.
XX
CC   A single-stranded DNA (or its complementary strand or the corresp.
CC   double-stranded DNA) which comprises one of the 7837 "GS" sequences
CC   given in AAT19001-T26837 and which is able to hybridise to part of
CC   human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
CC   sequences were obtained from 3'-directed cDNA libraries prepared
CC   from various human tissues; synthesis of cDNA was initiated from the
CC   3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
CC   untranslated sequence is unique to a particular mRNA species, almost
CC   all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
CC   is constructed so as to reflect accurately the relative abundance of
CC   different mRNAs in the particular tissue from which it was derived.
CC   The appearance frequency of a given GS in a cDNA library can be
CC   determined (esp. using primers and probes derived from the GS
CC   sequences) as a means of diagnosing abnormal cell function or for
CC   recognising different cell types.
XX
SQ   Sequence 350 BP; 54 A; 96 C; 115 G; 69 T; 16 other;


alignment_scores:
           Quality:    9.00            Length:      9
             Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-805-550-4 x AAT23970/rev   ..
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 Align seg 1/1  to reverse of: AAT23970  from: 1  to: 350

     234 AlaGlyGlyGlyAlaGlyGlyGlyPro 242
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      51 GCAGGTGGAGGTGCAGGGGGTGGGCCT 25

seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:AAX84178

seq_documentation_block:
ID   AAX84178 standard; cDNA; 440 BP.
XX
AC   AAX84178;
XX
DT   08-SEP-1999  (first entry)
XX
DE   DNA encoding human breast tumour protein immunogenic fragment.
XX
KW   Breast tumour protein; immunogenic fragment; vaccine; detection;
KW   breast cancer development; therapy; ss.
XX
OS   Homo sapiens.
XX
PN   WO9933869-A2.
XX
PD   08-JUL-1999.
XX
PF   22-DEC-1998;   98WO-US27416.
XX
PR   17-JUL-1998;   98US-0118627.
PR   24-DEC-1997;   97US-0998253.
PR   24-DEC-1997;   97US-0998255.
PR   17-JUL-1998;   98US-0118554.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Reed SG,  Xu J;
XX
DR   WPI; 1999-405486/34.
XX
PT   New breast tumour protein genes used, in vaccines for immunotherapy,
PT   or for diagnosis of breast cancer
XX
PS   Claim 12; Page 52; 70pp; English.
XX
CC   This sequence encodes a human breast tumour protein immunogenic fragment
CC   of the invention. The polypeptides or nucleic acids encoding them are
CC   useful in vaccines and pharmaceutical compositions for manufacture of
CC   medicaments for inhibiting the development of breast cancer in a patient.
CC   They can also be used to treat breast cancer. Antibodies against these
CC   polypeptides can be used to detect and monitor progression of breast
CC   cancer in patients. Primers and probes derived from the polynucleotides
CC   encoding the breast proteins are useful for detection of breast cancer.
CC   Peripheral blood cells from a patient incubated in the presence of at
CC   least one polypeptide, such that T cells proliferate, are useful in
CC   manufacture of a medicament for treating breast cancer in a patient.
CC   Antigen presenting cells incubated in the presence of at least one
CC   polypeptide are also useful for treating breast cancer.
XX
SQ   Sequence 440 BP; 70 A; 136 C; 137 G; 89 T; 8 other;


alignment_scores:
           Quality:    9.00            Length:      9
             Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-805-550-4 x AAX84178/rev   ..

 Align seg 1/1  to reverse of: AAX84178  from: 1  to: 440

     234 AlaGlyGlyGlyAlaGlyGlyGlyPro 242
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     83 GCAGGTGGAGGTGCAGGGGGTGGGCCT 57

seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:AAC79407

seq_documentation_block:
ID   AAC79407 standard; cDNA; 440 BP.
XX
AC   AAC79407;
XX
DT   07-FEB-2001  (first entry)
XX
DE   5' cDNA sequence of human breast tumour clone IE-4443.
XX
KW   Human; breast tumour antigen; cytostatic; immunotherapy;
KW   breast cancer; vaccine; ss.
XX
OS   Homo sapiens.
XX
PN   WO200061756-A2.
XX
PD   19-OCT-2000.
XX
PF   10-APR-2000; 2000WO-US09688.
XX
PR   09-APR-1999;   99US-0288950.
PR   02-JUL-1999;   99US-0346327.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Reed SG,  Xu J,  Dillon DC;
XX
DR   WPI; 2000-638568/61.
XX
PT   A novel isolated polypeptide comprising an immunogenic portion of a
PT   breast cancer protein useful in the detection and treatment of breast
PT   cancer -
XX
PS   Claim 13; Page 66-67; 95pp; English.
XX
CC   The present sequence was isolated from a breast tumour cDNA library. It
CC   is provided in a specification relating to compounds for immunotherapy
CC   and diagnosis of breast cancer. Breast tumour antigens and the
CC   polynucleotides that encode them may be used in the production of a
CC   pharmaceutical composition to be used in the treatment of breast cancer.
CC   Proliferated T cells and incubated antigen presenting cells are also
CC   required. The polypeptides and polynucleotides may also be used to
CC   produce a vaccine.
XX
SQ   Sequence 440 BP; 70 A; 136 C; 137 G; 89 T; 8 other;


alignment_scores:
            Quality:    9.00            Length:      9
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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 Align seg 1/1  to reverse of: AAC79407  from: 1  to: 440

     234 AlaGlyGlyGlyAlaGlyGlyGlyPro 242
         ||||||||||||||||||||||||||||
      83 GCAGGTGGAGGTGCAGGGGGTGGGCCT 57

seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:AAS80818

seq_documentation_block:
ID   AAS80818 standard; cDNA; 468 BP.
XX
AC   AAS80818;
XX
DT   13-FEB-2002  (first entry)
XX
DE   DNA encoding novel human diagnostic protein #16622.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT,  Liu C,  Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   P-PSDB; ABG16631.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity  -
XX
PS   Claim 1; SEQ ID No 16622; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. AAS64197-AAS94564 represent novel human
CC   diagnostic coding sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 468 BP; 92 A; 119 C; 119 G; 138 T; 0 other;


alignment_scores:
            Quality:    9.00            Length:      9
              Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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 Align seg 1/1  to: AAS80818  from: 1  to: 468

      80 SerGlySerThrGlyThrSerSerSer 88
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     404 TCGGGCTCCACCGGCACCTCGTCATCC 430

seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:AAC02213
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seq_documentation_block:
ID   AAC02213 standard; cDNA; 492 BP.
XX
AC   AAC02213;
XX
DT   06-OCT-2000  (first entry)
XX
DE   Human secreted protein 5' EST, SEQ ID NO: 2211.
XX
KW   Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW   gene therapy; chromosome mapping; ss.
XX
OS   Homo sapiens.
XX
PN   EP1033401-A2.
XX
PD   06-SEP-2000.
XX
PF   21-FEB-2000; 2000EP-0200610.
XX
PR   26-FEB-1999;   99US-0122487.
XX
PA   (GEST ) GENSET.
XX
PI   Dumas Milne Edwards J,  Duclert A,  Giordano J;
XX
DR   WPI; 2000-500381/45.
DR   P-PSDB; AAG02207.
XX
PT   New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT   obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT   diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
PS   Claim 1; SEQ ID 2211; 71pp + CD-ROM; English.
XX
CC   The present sequence is one of a large number of 5' ESTs derived from
CC   mRNAs encoding secreted proteins. An ORF has been identified within the
CC   sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
CC   derived from 30 different tissues. EST sequences usually correspond
CC   mainly to the 3' untranslated region (UTR) of the mRNA because they are
CC   often obtained from oligo-dT primed cDNA libraries. Such ESTs are not
CC   well suited for isolating cDNA sequences derived from the 5' ends of
CC   mRNAs and even in those cases where longer cDNA sequences have been
CC   obtained, the full 5' UTR is rarely included. 5' ESTs are derived from
CC   mRNAs with intact 5' ends and can therefore be used to obtain full length
CC   cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,
CC   gene therapy and chromosome mapping procedures. They are used to obtain
CC   upstream regulatory sequences and to design expression and secretion
CC   vectors.
XX
SQ   Sequence 492 BP; 152 A; 99 C; 160 G; 81 T; 0 other;


alignment_scores:
           Quality:    9.00            Length:      9
             Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-805-550-4 x AAC02213/rev   ..

 Align seg 1/1  to reverse of: AAC02213  from: 1  to: 492

      80 SerGlySerThrGlyThrSerSerSer 88
         |||||||||||||||||||||||||||
     116 TCGGGCTCCACCGGCACCTCGTCATCC 90
```